

CRF Errors Corrected by the STIC Systems Branch

Sortal Number: 09/975,063

**ENTERED**

CRF Processing Date: 11/6/2001  
 Edited by: [Signature]  
 Verified by: [Signature] (STIC stat)

- ☐ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;  
☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 2/1/95

## RAW SEQUENCE LISTING

DATE: 11/06/2001

PATENT APPLICATION: US/09/975,063

TIME: 08:01:49

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\11062001\I975063.raw

## SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: POWELL, Jerry S.

8 (ii) TITLE OF INVENTION: HUMAN ERYTHROPOIETIN GENE: HIGH LEVEL

9 EXPRESSION IN STABLY TRANSFECTED MAMMALIAN CELLS

11 (iii) NUMBER OF SEQUENCES: 6

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Dorsey & Whitney, LLP

15 (B) STREET: Suite 3400, 1420 Fifth Avenue, U.S. Bank Centre

16 (C) CITY: Seattle

17 (D) STATE: Washington

18 (E) COUNTRY: USA

19 (F) ZIP: 98101

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: WordPerfect 6/7/8

27 (vi) CURRENT APPLICATION DATA:

C--> 32 (A) APPLICATION NUMBER: US/09/975,063

C--> 33 (B) FILING DATE: 10-Oct-2001

35 (viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: Roberts, Mark W..

37 (B) REGISTRATION NUMBER: 46,160

38 (C) REFERENCE/DOCKET NUMBER: 500582.03 (112893.109)

40 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: 206-903-8728

42 (B) TELEFAX: 206-903-8820

45 (2) INFORMATION FOR SEQ ID NO: 1:

47 (i) SEQUENCE CHARACTERISTICS:

48 (A) LENGTH: 2426 base pairs

49 (B) TYPE: nucleic acid

50 (C) STRANDEDNESS: single

51 (D) TOPOLOGY: linear

53 (ii) MOLECULE TYPE: DNA (genomic)

58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

60	CCCGGTGTGG TCACCCGGCG CGCCCCAGGT CGCTGAGGGA CCCC GCCAG GCGCGGAGAT	60
62	GGGGGTGCAC GGTGAGTACT CGCGGGCTGG GCGCTCCCGC CCGCCCGGGT CCCTGTTTGA	120
64	GCGGGGATTT AGCGCCCCGG CTATTGGCCA GGAGGTGGCT GGGTTCAAGG ACCGGCGACT	180
66	TGTCAAGGAC CCCGGAAGGG GGAGGGGGGT GGGGCAGCCT CCACGTGCCA GCGGGGACTT	240
68	GGGGGAGTCC TTGGGGATGG CAAAAACCTG ACCTGTGAAG GGGACACAGT TTGGGGGTTG	300
70	AGGGGAAGAA GGTTTGGGGG GTTCTGCTGT GCCAGTGGAG AGGAAGCTGA TAAGCTGATA	360
72	ACCTGGGCGC TGGAGCCACC ACTTATCTGC CAGAGGGGAA GCCTCTGTCA CACCAGGATT	420
74	GAAGTTTGGC CGGAGAAGTG GATGCTGGTA GCCTGGGGGT GGGGTGTGCA CACGGCAGCA	480
76	GGATTGAATG AAGGCCAGGG AGGCAGCACC TGAGTGCTTG CATGGTTGGG GACAGGAAGG	540
78	ACGAGCTGGG GCAGAGACGT GGGGATGAAG GAAGCTGTCC TTCCACAGCC ACCCTTCTCC	600
80	CTCCCCGCCT GACTCTCAGC CTGGCTATCT GTTCTAGAAT GTCCTGCCTG GCTGTGGCTT	660

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82 CTCCTGTCCC TGCTGTGCGT CCCTCTGGGC CTCCCAGTCC TGGGCGCCCC ACCACGCCTC      720
84 ATCTGTGACA GCCGAGTCCT GCAGAGGTAC CTCTTGGAGG CCAAGAAGGC CGAGAATATC      780
86 ACGGTGAGAC CCCTTCCCCA GCACATTCCA CAGAACTCAC GCTCAGGGCT TCAGGGAAC      840
88 CCTCCAGAT CCAGGAACCT GGCACCTGGT TTGGGGTGGA GTTGGGAAGC TAGACACTGC      900
90 CCCCTACAT AAGAATAAGT CTGGTGGCCC CAAACCATAC CTGGAAACTA GGCAAGGAGC      960
92 AAAGCCAGCA GATCCTACGC CTGTGGCCAG GGCCAGAGCC TTCAGGGACC CTTGACTCCC     1020
94 CGGGCTGTGT GCATTTTACA CGGGCTGTGC TGAACACTGC AGCTTGAATG AGAATATCAC     1080
96 TGTCCAGAC ACCAAAGTTA ATTTCTATGC CTGGAAGAGG ATGGAGGTGA GTTCCTTTT      1140
98 TTTTTTTTTT CCTTCTTTT GGAGAAATCT ATTTGCGAGC CTGATTTTGG ATGAAAGGGA      1200
100 GAATGATCGA GGGAAAGGTA AAATGGAGCA GCAGAGATGA GGCTGCCTGG GCGCAGAGGC     1260
102 TCACGTCTAT AATCCCAGGC TGAGATGGCC GAGATGGGAG AATTGCTTGA GCCCCGGAGT     1320
104 TTCAGACCAA CCTAGGAGC ATAGTGAGAT CCCCCTCTC TACAAACATT TAAAAAATT      1380
106 AGTCAGGTGA AGTGGTGCAT GGTGGTAGTC CCAGATATTT GGAAGGCTGA GCGGGGAGGA     1440
108 TCGCTGGAGC CCAGGAATTT GAGGCTGCAG TGAGCTGTGA TCACACCACT GAACTCCAGC     1500
110 CTCAGTGACA GAGTGAGGCC CTGTCTCAA AAAGAAAAGA AAAAAAGAAA ATAATGAGGG     1560
112 CTGTATGAA TACGTTTATT ATTCATTCAC TCACTCACTC ACTCATTCAT TCATTTCATT     1620
114 ATTCAACAAG TCTTATTGCA TACCTTCTGT TTGCTCAGCT TGGTGCTTGG GGCTGCTGAG     1680
116 GGGCAGGAGG GAGAGGGTGA CATCCCTCAG CTGACTCCCA GAGTCCACTC CCTGTAGGTC     1740
118 GGGCAGCAGG CCGTAGAAGT CTGGCAGGGC CTGGCCCTGC TGTGCGAAGC TGTCTGCGG     1800
120 GGCCAGGCCC TGTGTTGTA CTCTTCCCAG CCGTGGGAGC CCCTGCAGCT GCATGTGGAT     1860
122 AAAGCCGTCA GTGGCCTTCG CAGCCTCACC ACTCTGCTTC GGGCTCTGGG AGCCCAGGTG     1920
124 AGTAGGAGCG GACACTTCTG CTTGCCCTTT CTGTAAGAAG GGGAGAAGGG TCTTGCTAAG     1980
126 GAGTACAGGA ACTGTCCGTA TTCTTCCCT TTCTGTGGCA CTGCAGCGAC CTCCTGTTTC     2040
128 CTCCTTGGCA GAAGGAAGCC ATCTCCCTC CAGATGCGGC CTCAGCTGCT CCACTCCGAA     2100
130 CAATCACTGC TGACACTTTC CGCAAACCT TCCGAGTCTA CTCCAATTT CTCCGGGGAA     2160
132 AGCTGAAGCT GTACACAGGG GAGGCCTGCA GGACAGGGGA CAGATGACCA GGTGTGTCCA     2220
134 CCTGGGCATA TCCACCACCT CCCTCACCAA CATTGCTTGT GCCACACCCT CCCCAGCCAC     2280
136 TCCTGAACCC CGTCGAGGGG CTCTCAGCTC AGCGCCAGCC TGTCCCATGG ACACTCCAGT     2340
138 GCCACCAATG ACATCTCAGG GGCCAGAGGA ACTGTCCAGA GAGCAACTCT GAGATCTAAG     2400
140 GATGTACAG GGCCAACTTG AGGGCC      2426
142 (2) INFORMATION FOR SEQ ID NO: 2:
144     (i) SEQUENCE CHARACTERISTICS:
145         (A) LENGTH: 30 amino acids
146         (B) TYPE: amino acid
147         (C) STRANDEDNESS: single
148         (D) TOPOLOGY: linear
150     (ii) MOLECULE TYPE: peptide
155     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
W--> 157   Ala Pro Xaa Arg Leu Ile Leu Asp Ser Arg Val Leu Glu Arg Tyr Leu
158       1         5         10         15
W--> 160   Leu Glu Ala Lys Glu Ala Glu Xaa Ile Thr Asp Gly Gly Ala
161       20         25         30
163 (2) INFORMATION FOR SEQ ID NO: 3:
165     (i) SEQUENCE CHARACTERISTICS:
166         (A) LENGTH: 7 amino acids
167         (B) TYPE: amino acid
168         (C) STRANDEDNESS: single
169         (D) TOPOLOGY: linear
171     (ii) MOLECULE TYPE: peptide

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176 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
178 Glu Ala Lys Glu Ala Glu Asn  
179 1 5

181 (2) INFORMATION FOR SEQ ID NO: 4:  
183 (i) SEQUENCE CHARACTERISTICS:  
184 (A) LENGTH: 20 base pairs  
185 (B) TYPE: nucleic acid  
186 (C) STRANDEDNESS: single  
187 (D) TOPOLOGY: linear  
189 (ii) MOLECULE TYPE: DNA (genomic)

194 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
196 TTYTCDGCTT CYTTDGCTTC 20

198 (2) INFORMATION FOR SEQ ID NO: 5:  
200 (i) SEQUENCE CHARACTERISTICS:  
201 (A) LENGTH: 6 amino acids  
202 (B) TYPE: amino acid  
203 (C) STRANDEDNESS: single  
204 (D) TOPOLOGY: linear  
206 (ii) MOLECULE TYPE: peptide

211 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
213 Glu Asn Ile Thr Asp Gly  
214 1 5

216 (2) INFORMATION FOR SEQ ID NO: 6:  
218 (i) SEQUENCE CHARACTERISTICS:  
219 (A) LENGTH: 23 base pairs  
220 (B) TYPE: nucleic acid  
221 (C) STRANDEDNESS: single  
222 (D) TOPOLOGY: linear  
224 (ii) MOLECULE TYPE: DNA (genomic)

229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
231 AGCTCCTCCA TCAGTATTAT TTY 23

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/975,063

DATE: 11/06/2001

TIME: 08:01:50

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\11062001\I975063.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2